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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/024,066	12/18/2001	Loren J. Field	7037-450	3713

7590 07/20/2005

Kenneth A. Gandy  
Woodard, Emhardt, Naughton, Moriarty & McNett  
Bank One Center/Tower, Suite 3700  
111 Monument Circle  
Indianapolis, IN 46204-5137

EXAMINER

SULLIVAN, DANIEL M

ART UNIT PAPER NUMBER

1636

DATE MAILED: 07/20/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

## Office Action Summary

**Application No.**

10/024,066

**Applicant(s)**

FIELD ET AL.

**Examiner**

Daniel M. Sullivan

**Art Unit**

1636

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

### Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

### Status

- 1) ☒ Responsive to communication(s) filed on 06 July 2005.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

### Disposition of Claims

- 4) ☒ Claim(s) 51 and 52 is/are pending in the application.
- 4a) Of the above claim(s) \_\_\_\_\_ is/are withdrawn from consideration.
- 5) ☐ Claim(s) \_\_\_\_\_ is/are allowed.
- 6) ☒ Claim(s) 51 and 52 is/are rejected.
- 7) ☐ Claim(s) \_\_\_\_\_ is/are objected to.
- 8) ☐ Claim(s) \_\_\_\_\_ are subject to restriction and/or election requirement.

### Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on \_\_\_\_\_ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.  
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).  
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

### Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some \* c) ☐ None of:
- ☐ Certified copies of the priority documents have been received.
  - ☐ Certified copies of the priority documents have been received in Application No. \_\_\_\_\_.
  - ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

\* See the attached detailed Office action for a list of the certified copies not received.

### Attachment(s)

- |  |   |
|--|---|
| 1) <input checked="" type="checkbox"/> Notice of References Cited (PTO-892)  | 4) <input checked="" type="checkbox"/> Interview Summary (PTO-413)<br>Paper No(s)/Mail Date. <u>7/12/05</u> |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948)                                   | 5) <input type="checkbox"/> Notice of Informal Patent Application (PTO-152)                                 |
| 3) <input type="checkbox"/> Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)<br>Paper No(s)/Mail Date _____ | 6) <input checked="" type="checkbox"/> Other: <u>sequence alignments</u> .                                  |

### **DETAILED ACTION**

This Non-Final Office Action is a response to the Paper filed 6 July 2005 in response to the Final Office Action mailed 8 February 2005. Claims 43-59 and 63-84 had been withdrawn from consideration and claims 20-28, 49, 50 and 51-62 were considered in the 8 February Office Action. Claims 20-28, 49, 50, 53-62 and 63-84 were canceled and claims 51 and 52 were amended in the 6 July Paper. Claims 51 and 52 are pending.

Finality of the previous Office Action is hereby **withdrawn** in view of the new grounds for rejection set forth herein below.

#### ***Response to Amendment***

Rejection of claims 20-28, 49, 50 and 53-62 is rendered moot by the cancellation thereof.

Objection to claims 51 and 52 is withdrawn in view of the amendments thereto.

#### ***Claim Rejections - 35 USC § 103***

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negated by the manner in which the invention was made.

The factual inquiries set forth in *Graham v. John Deere Co.*, 383 U.S. 1, 148 USPQ 459 (1966), that are applied for establishing a background for determining obviousness under 35 U.S.C. 103(a) are summarized as follows:

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1. Determining the scope and contents of the prior art.
2. Ascertaining the differences between the prior art and the claims at issue.
3. Resolving the level of ordinary skill in the pertinent art.
4. Considering objective evidence present in the application indicating obviousness or nonobviousness.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

Claim 51 is rejected under 35 U.S.C. 103(a) as being unpatentable over Soonpaa *et al.* (1997) *J. Clin. Invest.* 99:2644 (previously made of record) in view of Li *et al.* (1998) *Am. J. Physiol.* 275:H814-H822 and further in view of ENTREZ Nucleotide Database Entry Accession No. M86182 (hereinafter, M86182).

The claim is directed to a cardiomyocyte cell including an introduced nucleic acid molecule wherein the molecule encodes the polypeptide set forth as SEQ ID NO: 2.

Soonpaa *et al.* teaches overexpression of a cyclin D protein in cardiomyocytes of a transgenic mouse (see especially the paragraph bridging the left and right columns on page 2645 and the paragraph bridging the left and right columns on page 2647).

Soonpaa does not teach overexpression of an introduced nucleic acid encoding a nucleic acid comprising the amino acid sequence of SEQ ID NO: 2. However, Soonpaa *et al.* teaches, “[g]iven the therapeutic potential of regenerative myocardial growth, considerable effort has

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been invested to develop strategies to induce cardiomyocyte proliferation” (first full paragraph in the left column on page 2644) and “[t]his study represents an initial pragmatic effort to test candidate genes which may participate in the regulation of cardiomyocyte DNA synthesis” (third paragraph on page 2645).

Li *et al.* teaches that cyclin D2 is upregulated during cardiomyocyte hypertrophic growth (see especially the Abstract, the paragraph bridging pages H816-H817, Figure 2 and the caption thereto). Li *et al.* concludes, “[f]uture experiments designed to induce forced expression of these [including cyclin D2] molecules in cardiomyocytes should offer an approach to determine the precise role of cell cycle regulatory molecules in cardiomyocyte hypertrophy and may lead to strategies for improving the prognosis of this disease” (paragraph bridging pages H821-H822).

M86182 teaches a cyclin D2 nucleic acid encoding the instant SEQ ID NO: 2 (see the attached sequence alignment).

It would have been obvious to one of ordinary skill in the art at the time the invention was made to produce a transgenic mouse according to the teachings of Soonpaa *et al.* using the cyclin D2 nucleic acid disclosed in M86182 the cardiomyocytes of which would be the same as the cardiomyocytes of the instant claims. Motivation to combine these teachings comes from Soonpaa *et al.*, who teaches the desirability of identifying regulators of cardiomyocyte proliferation and that the transgenic animal disclosed therein provides a means to test candidate genes that may participate in regulation of cardiomyocyte DNA synthesis. Further motivation comes from the teachings of Li *et al.*, which establish the upregulation of cyclin D2 during cardiomyocyte hypertrophic growth and teach that forced overexpression of genes upregulated in hypertrophy should offer an approach to determine the role of these genes and may lead to

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therapeutic strategies. Thus, the skilled artisan would clearly be motivated to make a mouse comprising a nucleic acid encoding the instant SEQ ID NO: 2 as disclosed in M86182.

Absent evidence to the contrary, one would have a reasonable expectation of success in combining these teachings in view of the well-established nature of transgenic animal technology and the guidance for making a transgenic animal expressing a cyclin D protein provided in Soonpaa *et al.*

For these reasons, the invention of claim 51, as a whole, would have been obvious to one of ordinary skill in the art at the time the invention was made.

Claim 52 is rejected under 35 U.S.C. 103(a) as being unpatentable over Soonpaa *et al.* (1997) *J. Clin. Invest.* 99:2644 (previously made of record) in view of Li *et al.* (1998) *Am. J. Physiol.* 275:H814-H822 and further in view of ENTREZ Nucleotide Database Entry Accession No. X68452 (hereinafter, X68452).

The claim is directed to a cardiomyocyte cell including an introduced nucleic acid molecule wherein the molecule encodes the polypeptide set forth as SEQ ID NO: 4.

Soonpaa *et al.* teaches overexpression of a cyclin D protein in cardiomyocytes of a transgenic mouse (see especially the paragraph bridging the left and right columns on page 2645 and the paragraph bridging the left and right columns on page 2647).

Soonpaa does not teach overexpression of an introduced nucleic acid encoding a nucleic acid comprising the amino acid sequence of SEQ ID NO: 4. However, Soonpaa *et al.* teaches, “[g]iven the therapeutic potential of regenerative myocardial growth, considerable effort has been invested to develop strategies to induce cardiomyocyte proliferation” (first full paragraph in

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the left column on page 2644) and “[t]his study represents an initial pragmatic effort to test candidate genes which may participate in the regulation of cardiomyocyte DNA synthesis” (third paragraph on page 2645).

Li *et al.* teaches that cyclin D2 is upregulated during cardiomyocyte hypertrophic growth (see especially the Abstract, the paragraph bridging pages H816-H817, Figure 2 and the caption thereto). Li *et al.* concludes, “[f]uture experiments designed to induce forced expression of these [including cyclin D2] molecules in cardiomyocytes should offer an approach to determine the precise role of cell cycle regulatory molecules in cardiomyocyte hypertrophy and may lead to strategies for improving the prognosis of this disease” (paragraph bridging pages H821-H822).

X68452 teaches a cyclin D2 nucleic acid encoding the instant SEQ ID NO: 4 (see the attached sequence alignment).

It would have been obvious to one of ordinary skill in the art at the time the invention was made to produce a transgenic mouse according to the teachings of Soonpaa *et al.* using the cyclin D2 nucleic acid disclosed in X68452, the cardiomyocytes of which would be the same as the cardiomyocytes of the instant claims. Motivation to combine these teachings comes from Soonpaa *et al.*, who teaches the desirability of identifying regulators of cardiomyocyte proliferation and that the transgenic animal disclosed therein provides a means to test candidate genes that may participate in regulation of cardiomyocyte DNA synthesis. Further motivation comes from the teachings of Li *et al.*, which establish the upregulation of cyclin D2 during cardiomyocyte hypertrophic growth and teach that forced overexpression of genes upregulated in hypertrophy should offer an approach to determine the role of these genes and may lead to

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therapeutic strategies. Thus, the skilled artisan would clearly be motivated to make a mouse comprising a nucleic acid encoding the instant SEQ ID NO: 4 as disclosed in X68452.

Absent evidence to the contrary, one would have a reasonable expectation of success in combining these teachings in view of the well-established nature of transgenic animal technology and the guidance for making a transgenic animal expressing a cyclin D protein provided in Soonpaa *et al.*

For these reasons, the invention of claim 52, as a whole, would have been obvious to one of ordinary skill in the art at the time the invention was made.


### ***Conclusion***

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Daniel M Sullivan whose telephone number is 571-272-0779. The examiner can normally be reached on Monday through Friday 6:30-3:00.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Remy Yucel, Ph.D. can be reached on 571-272-0781. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Daniel M. Sullivan, Ph.D.  
Examiner  
Art Unit 1636

  
**DANIEL M. SULLIVAN**  
**PATENT EXAMINER**



QY	261	TyArgGlnAspGlnArgAspGlySerLysSerGluAspGluLeuAspGlnAlaSerThr	280
Db	936	TACCGTCAGACCAACAGTCGACGATCCAGTCGAGGATGAATGAGCAAGCCAGCACC	995
QY	281	ProThrAspValArgAspLeu 289	
Db	996	CCTACAGACGTGGGATATCGACCTG 1022	
RESULT 3			
HSCYCD2			
LOCUS	HSCYCD2	1129 bp	mRNA
DEFINITION	H.sapiens mRNA for cyclin D2.		linear
ACCESSION	X68452		PRI 30-MAR-1993
VERSION	X68452.1	GI:38415	
KEYWORDS	binding protein; CND2 gene; cyclin D2; protein kinase.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Palmero, I., Holder, A., Sinclair, A.J., Dickson, C. and Peters, G.		
TITLE	Cyclins D1 and D2 are differentially expressed in human B-lymphoid cell lines		
JOURNAL	Oncogene 8 (4), 1049-1054 (1993)		
MEDLINE	93205384		
PUBMED	8455931		
REFERENCE	2 (bases 1 to 1129)		
AUTHORS	Peters, G.		
TITLE	Direct Submission		
JOURNAL	Submitted (17-SEP-1992) G. Peters, Imperial Cancer Research Fund, P.O.Box 123, Lincoln's Inn Fields, London WC2A 3PX, UK		
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ORIGIN			
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Pred. No.:	1.33e-146	Length:	1129
Score:	1501.00	Matches:	289
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
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US-10-024-066-4 (1-289) x HSCYCD2 (1-1129)			
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QY	21	LeuArgAspAspArgValLeuGlnAsnLeuLeuThrIleGluGluArgTyrLeuProGln	40

Db	216	CTCCGAGACGACCGCTCTGCAGAACCTGCTCACCATCGAGGAGCGCTACCTTCGCGAG	275
QY	41	CysSerTyrPheLysCysValGlnLysAspIleGlnProTyrMetArgArgMetValAla	60
Db	276	TGCTCTACTTCAAGTCGCTGCAGAGGACATCCACCTACATGCGCAGATGGTGGCC	335
QY	61	ThrTrpMetLeuGluValCysGluGluGlnLysCysGluGluValPheProLeuAla	80
Db	336	ACCTGGATGCTGGAGGCTGTGTGAGGAACAGAGTGCAGAGAGAGGTCTTCCCTCTGGCC	395
QY	81	MetAsnTyrLeuAspArgPheLeuAlaGlyValProThrProLysSerHisLeuGlnLeu	100
Db	396	ATGAATTACTGGACCGTTTCTTGGCTGGGGTCCGACTCCGAAGTCCCATCTGCAACTC	455
QY	101	LeuGlyValaValCysMetPheLeuAlaSerLysLeuLysGluThrSerProLeuThrAla	120
Db	456	CTGGGTGCTGTCTGCATGTTCCTGGCTCCAACTCAAGAGACCCGCTGACCGCG	515
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Db	516	GAGAGCTGTGCATTTACACCGACAACTCCATCAGCTCAGGAGCTGTGAGTGGAA	575
QY	141	LeuValValLeuGlyLysLeuLysTrpAsnLeuAlaAlaValThrProHisAspPheIle	160
Db	576	CTGGTGTGCTGGGGAAGTTGAAGTGGAACTGGCAGCTGTCTCTCATGACTTCATT	635
QY	161	GluHisIleLeuArgLysLeuProGlnGlnArgGluLysLeuSerLeuIleArgLysHis	180
Db	636	GAGCATCTTGGGAGAGCTGCCAGCAGCGGAGAGAGCTGTCTCTGATCCGACGAT	695
QY	181	AlaGlnThrPheIleAlaLeuCysAlaThrAspPheLysPheAlaMetTyrProSer	200
Db	696	GCTCAGACCTTCATTGCTCTGTGTGCCACCGACTTTTAAGTTTGCCATGTACCCACGCTG	755
QY	201	MetIleAlaThrGlySerValGlyAlaAlaIleCysGlyLeuGlnGlnAspGluVal	220
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QY	221	SerSerLeuThrCysAspAlaLeuThrGluLeuLeuAlaLysIleThrAsnThrAspVal	240
Db	816	AGCTGCTCCTGTGTGATGCCCTGTGAGCTGTGCTTAAAGTATCAACACACAGAGCTG	875
QY	241	AspCysLeuLysAlaCysGlnGluGlnIleGluAlaValLeuLeuAsnSerLeuGlnGln	260
Db	876	GATTGTCTCAAGCTTGCCAGGAGCAGATTGAGGCGGTGCTCTCTCAATAGCTCGACAG	935
QY	261	TyrArgGlnAspGlnArgAspGlySerLysSerGluAspGluLeuAspGlnAlaSerThr	280
Db	936	TACCGTCAGGACCAACGTCAGCGATCCAAAGTCGGAGGATGAATGAGCAAGCCAGCACC	995
QY	281	ProThrAspValArgAspIleAspLeu 289	
Db	996	CCTACAGACGTGGGATATCGACCTG 1022	

BC010958	1344 bp	mRNA	linear	PRI 29-JUN-2004
Homo sapiens cyclin D2, mRNA (cDNA clone MGC:13641 IMAGE:4133621), complete cds.				
ACCESSION	BC010958			
VERSION	BC010958.1	GI:15012104		
KEYWORDS	MGC.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	1 (bases 1 to 1344)			
	Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altshuler, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heish, P., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,			

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Db      405 AATTACCTGGACCGTTTCTTGCTGGAGTCCCGACTCTTAAGACCACTTTCAGTCTCTG 464
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Qy      121 LysLeuCysIleTyrThrAspAsnSerValIysProGlnGluLeuLeuGluThrIle 140
Db      525 AAGCTGTGCATTTACACGACAACTCTGTGAAGCCCGCAGGAGCTCTGAGTGGGAACCTG 584
Qy      141 ValValLeuGlyLysLeuLysIleAsnLeuAlaValThrProHisAspPheIleGlu 160
Db      585 GTAGTGTGGTAACTGAGTGGAACTTGGCCGCGAGTCAACCTTCACGACTTCATTGAG 644
Qy      161 HisLeuLeuArgLysLeuProGlnGlnLysGluLysLeuSerLeuIleArgLysHisAla 180
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Qy      181 GlnThrPheIleAlaLeuCysAlaThrAspPheLysPheAlaMetTyrProProSerMet 200
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Qy      221 ThrLeuThrCysAspAlaLeuThrGluLeuLeuAlaIleThrHisThrAspValAsp 240
Db      825 ACATCTACGTGTGATGCTGCTGAGTGGCTGTGGCCAAAGATCAACCCACACTGATGATG 884
Qy      241 CysLeuLysAlaCysGlnGlnGlnIleGluAlaLeuLeuLeuAsnSerLeuGlnPhe 260
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Qy      261 ArgGlnGluGlnHisAsnAlaGlySerLysSerValGluAspProAspGlnAlaThrThr 280
Db      945 CGTCAAGAGCAGCAATACCGGATCCCAAGTCTGTGGAGATCCGACCAAGCCACCACC 1004
Qy      281 ProThrAspValArgAspValAspLeu 289
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RESULT 3
LOCUS      AX695627      1255 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION Sequence 1254 from Patent WO03008583.
ACCESSION  AX695627
VERSION     AX695627.1  GI:29418779
KEYWORDS    Mus musculus (house mouse)
SOURCE      Mus musculus
ORGANISM    Mus musculus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE   1
AUTHORS     Morris,D.W. and Engelhard,E.K.
TITLE       Novel compositions and methods for cancer
JOURNAL     Patent: WO 03008583-A 1254 30-JAN-2003;
            Sagres Discovery (US)
FEATURES    Location/Qualifiers
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## FEATURES

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Score:          1513.00      Matches:    289
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:    0
DB:              Gaps:      0

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## ORIGIN

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MUSDCYC      MUSDCYC      1255 bp      mRNA      linear      ROD 27-APR-1993
DEFINITION   Mouse D-type cyclin (CYL2) mRNA, complete cds.
ACCESSION    M83749
VERSION      M83749.1  GI:192938
KEYWORDS     D-type cyclin.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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## RESULT 4

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MUSDCYC      MUSDCYC      1255 bp      mRNA      linear      ROD 27-APR-1993
DEFINITION   Mouse D-type cyclin (CYL2) mRNA, complete cds.
ACCESSION    M83749
VERSION      M83749.1  GI:192938
KEYWORDS     D-type cyclin.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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US-10-024-066-2 (1-289) x AX695627 (1-1255)

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Qy      1  MetGluLeuLeuCysCysGluValAspProValArgAlaValProAspArgAsnLeu 20
Db      271 ATGGAGCTGCTGTGCTGGAGGTGGACCCGGTCCGACGGGCGTCCGGACCGCAACCTG 330
Qy      21  LeuGluAspArgValLeuGlnAsnLeuThrIleGluGluArgTyrIleuProGlnCys 40
Db      331 CTGGAAGACCGCGTCTTCAGAACCTGTTGACCATCGAGGAGCGCTACCTCCGCGAGTGT 390
Qy      41  SerTyrPheLysCysValGlnLysAspIleGlnProTyrMetArgArgMetValAlaThr 60
Db      391 TCCATATTTCAAGTGGTGGTGGAGAGACATCCAAACGTTACATGCGGAGATGGTGCCACC 450
Qy      61  TrpMetLeuGluValCysGluGluGlnLysCysGluGluGluValPheProLeuAlaMet 80
Db      451 TGGATGCTAGAGGCTCTGTGAGGACAAAGTGTGAGAGAGAGGTCTTTCTCTGCGCCATG 510
Qy      81  AsnTyrIleAspArgPheLeuAlaGlyValProThrProLysThrHisLeuGlnLeuLeu 100
Db      511 AATTACCTGGACCGTTTCTTGCTGGAGTCCCGACTCTCTAAGACCCATCTTCAGTCTCTG 570
Qy      101 GlyAlaValCysMetPheLeuAlaSerIysLeuLysGluThrIleProLeuThrAlaGlu 120
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Qy      121 LysLeuCysIleTyrThrAspAsnSerValIysProGlnGluLeuLeuGluThrIleGlu 140
Db      631 AAGCTGTGCATTTACACGCAACTCTGTGAGGCCCGCAGGAGCTGCTGGAGTGGGACCTG 690
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Qy      221 ThrLeuThrCysAspAlaLeuThrGluLeuLeuAlaLysIleThrHisThrAspValAsp 240
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Qy      241 CysLeuLysAlaCysGlnGlnGlnIleGluAlaLeuLeuLeuAsnSerLeuGlnGlnPhe 260
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Qy      281 ProThrAspValArgAspValAspLeu 289
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QY 121 LysLeuCysIleTyrThrAspAsnSerValLysProGlnGluLeuGluTrpGluLeu 140  
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QY 281 ProThrAspValArgAspValAspLeu 289  
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## RESULT 2

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 ACCESSION  
 M86182  
 VERSION  
 M86182.1 GI:192879  
 FEATURES  
 cyclin 2.  
 Mus musculus (house mouse)

ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE  
 1 (bases 1 to 1034)  
 Matsuhashime,H., Roussel,M.F., Ahmun,R.A. and Sherr,C.J.  
 Colony-stimulating factor 1 regulates novel cyclins during the G1  
 phase of the cell cycle  
 CELL 65 (4), 701-713 (1991)  
 JOURNAL  
 MEDLINE  
 91235305  
 PUBMED  
 1827757  
 REFERENCE  
 2 (bases 1 to 1034)  
 Matsuhashime,H., Roussel,M.F. and Sherr,C.J.  
 Novel mammalian cyclin (CYL genes) expressed during G1  
 Unpublished.  
 JOURNAL  
 COMMENT  
 Original source text: Mus musculus (sub\_species domesticus) cDNA to  
 mRNA.

## FEATURES

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## ORIGIN

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 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 10 Gaps: 0  
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QY 21 LeuGluAspArgValLeuGlnAsnLeuThrIleGluGluArgTyrLeuProGlnCys 40  
 DB 225 CTGGAGACCGGCTTCTGCGAGACCTGTTGACCATGAGGAGGCTACCTCCCGCAGTGT 284

QY 41 SerTyrPheLysCysValGlnLysAspIleGlnProTyrMetArgArgMetValAlaThr 60  
 DB 285 TCTATTTCAGTGGCTGCGAGAGGACATCCACCGTACATGCGCAGGATGTGGCCACC 344

QY 61 TrpMetLeuGluValCysGluGluGlnLysCysGluGluValPheProLeuAlaMet 80  
 DB 601 TGGATGCTAGAGGCTCTGTGAGGACAAAGTGTGAAGAGAGCTCTTCTCTGGCCATG 860

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 13, 2005, 23:40:22 ; Search time 569.5 Seconds  
(without alignments)  
2710.137 Million cell updates/sec

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Searched: 6330947 seqs, 3139163630 residues

Total number of hits satisfying chosen parameters: 13661894

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

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7	1380	91.2	1898	22	US-10-309-035-14
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ALIGNMENTS

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; Sequence 3, Application US/09997722  
; Publication No. US20040072154A1  
; GENERAL INFORMATION:  
; APPLICANT: Morris, David  
; APPLICANT: Engelhard, Eric  
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER  
; FILE REFERENCE: A-71171/RMS/DCF  
; CURRENT APPLICATION NUMBER: US/09/997,722  
; CURRENT FILING DATE: 2001-11-30  
; PRIOR APPLICATION NUMBER: US 09/747,377  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 09/798,586  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 301

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 13, 2005, 20:22:56 ; Search time 189 Seconds  
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2502.032 Million cell updates/sec

Title: US-10-024-066-2

Perfect score: 1513

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Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1380	91.2	6478	4	US-09-919-497-4
5	1380	91.2	6478	4	US-09-943-016-256
6	1380	91.2	6479	4	US-09-949-016-2149
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8	1357	89.7	1970	3	US-08-463-772-3
9	1357	89.7	1970	5	PCT-US93-05000-3
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15	958	63.3	4221	3	US-08-947-492-7	Sequence 7, Appli
16	958	63.3	4242	4	US-09-023-655-1365	Sequence 1365, Ap
17	958	63.3	4244	2	US-08-460-694-1	Sequence 1, Appli
18	958	63.3	4244	3	US-08-460-744-1	Sequence 1, Appli
19	958	63.3	4244	3	US-07-667-711B-1	Sequence 1, Appli
20	957	63.3	4453	1	US-08-770-761A-4	Sequence 4, Appli
21	957	63.3	4540	1	US-08-770-761A-6	Sequence 6, Appli
22	957	63.3	4621	1	US-08-770-761A-1	Sequence 1, Appli
23	951.5	62.9	1462	5	PCT-US93-05000-30	Sequence 30, Appl
24	946	62.9	1325	1	US-08-306-691B-51	Sequence 51, Appl
25	916.5	60.6	1962	2	US-08-246-361A-5	Sequence 5, Appli
26	916.5	60.6	1962	4	US-09-023-655-1023	Sequence 1023, Ap
27	916.5	60.6	2042	4	US-09-814-915A-59	Sequence 59, Appl
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30	892	59.0	1325	3	US-08-463-772-1	Sequence 1, Appli
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38	428.5	28.3	1901	5	PCT-US93-05000-32	Sequence 32, Appl
39	372.5	24.6	36302	4	US-09-949-016-11998	Sequence 11998, A
40	372.5	24.6	36302	4	US-09-949-016-13891	Sequence 13891, A
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C 44	321.5	21.2	32207	3	US-09-230-371A-20	Sequence 20, Appl
45	276	18.2	601	4	US-09-949-016-23242	Sequence 23242, A

ALIGNMENTS

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; Patent No. 6492173  
; GENERAL INFORMATION:  
; APPLICANT: Lex M. Cowsett  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CYCLIN D2 EXPRESSION  
; FILE REFERENCE: RTS-0275  
; CURRENT APPLICATION NUMBER: US/09/920,760  
; CURRENT FILING DATE: 2001-08-01  
; NUMBER OF SEQ ID NOS: 89  
; SEQ ID NO 3  
; LENGTH: 1129  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (156)...(1025)  
US-09-920-760-3

Alignment Scores:  
Pred. No.: 3,15e-180 Length: 1129  
Score: 1380.00 Matches: 266  
Percent Similarity: 97.24% Conservative: 16  
Best Local Similarity: 91.72% Mismatches: 6  
Query Match: 91.21% Indels: 2  
DB: 4 Gaps: 2

US-10-024-066-2 (1-289) x US-09-920-760-3 (1-1129)

Qy	1	MetGluLeuLeuCysGluValAspProValArgAlaValProAspArgAsnLeu	20
Db	156	ATGGAGCTGCTGTGGCCACGAGGTGGACCCCGTCCGAGGGCCGTGGCGGACCGACCTG	215
Qy	21	Leu---GluAspArgValLeuGlnAsnLeuLeuThrIleGluArgTyrLeuProGln	39
		:::	

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 13, 2005, 17:34:44 ; Search time 596.5 Seconds  
(without alignments)  
2868.072 Million cell updates/sec

Title: US-10-024-066-2

Perfect score: 1513

Sequence: 1 MELLCCVDPVRRVAPDRNL.....KSVDPDQATPTDVRVDL 289

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-O=/cgn2\_1/USPTO\_spool\_h/US10024066/runat\_13072005\_140959\_28036/app\_query.fasta\_1.910  
-DB=N\_Geneseq -QFWT=fastcap -SURFIX=ring -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=BLOSUM62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10024066 @CIGN 1.1 586 @runat\_13072005\_140959\_28036 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N Geneseq\_16Dec04:\*  
1: Geneseq\_1980s:\*  
2: Geneseq\_1990s:\*  
3: Geneseq\_2000s:\*  
4: Geneseq\_2001as:\*  
5: Geneseq\_2001bs:\*  
6: Geneseq\_2002as:\*  
7: Geneseq\_2002bs:\*  
8: Geneseq\_2003as:\*  
9: Geneseq\_2003bs:\*  
10: Geneseq\_2003cs:\*  
11: Geneseq\_2003ds:\*  
12: Geneseq\_2004as:\*  
13: Geneseq\_2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1513	100.0	870	9 ADA02737	Ada02737 Mouse Ccn
2	1513	100.0	870	10 ADB72475	Adb72475 Mouse Ccn
3	1513	100.0	870	10 ADC85217	Adc85217 Mouse Ccn
4	1513	100.0	870	12 ADM74332	Adm74332 Murine ca
5	1513	100.0	876	5 AAD02406	Aad02406 Mouse cys

6	1513	100.0	1255	9 ADA02736	Ada02736 Mouse Ccn
7	1513	100.0	1255	10 ADB72474	Adb72474 Mouse Ccn
8	1513	100.0	1255	10 ADC85216	Adc85216 Mouse Ccn
9	1513	100.0	1255	12 ADM74331	Adm74331 Murine ca
10	1380	91.2	870	9 ADA02740	Ada02740 Human Ccn
11	1380	91.2	870	10 ADB72478	Adb72478 Human Ccn
12	1380	91.2	870	10 ADC85220	Adc85220 Human Ccn
13	1380	91.2	870	12 ADM74335	Adm74335 Human car
14	1380	91.2	873	5 AAD02407	Aad02407 Human cnc
15	1380	91.2	1129	10 ACA60565	ACA60565 DNA encod
16	1380	91.2	1898	10 ADD18442	Ad18442 Human pro
17	1380	91.2	1911	2 AAQ31874	Aaq31874 Cyclin D2
18	1380	91.2	1911	11 ADI31696	Adi31696 Human cDN
19	1380	91.2	6478	6 ABK35484	Abk35484 Human end
20	1380	91.2	6478	6 ABL66613	Ab166613 Lung canc
21	1380	91.2	6478	6 ABV94470	Abv94470 Breast ca
22	1380	91.2	6478	6 ABN95109	Abn95109 Gene #160
23	1380	91.2	6478	9 ADA02739	Ada02739 Human Ccn
24	1380	91.2	6478	10 ADB72477	Adb72477 Human Ccn
25	1380	91.2	6478	10 ADC85219	Adc85219 Human Ccn
26	1380	91.2	6478	10 ADH28853	Adh28853 Human chr
27	1380	91.2	6478	10 ADH28853	Adh28853 Human chr
28	1380	91.2	6478	12 ADM74334	Adm74334 Human car
29	1380	91.2	6478	12 ADOL9119	Ado19119 Human PRO
30	1380	91.2	6480	8 ACF34507	Acf34507 Gene enco
31	1380	91.2	6480	10 ADF76507	Adf76507 Novel hum
32	1380	91.2	6480	12 ADH17148	Adh17148 Human cyc
33	1380	91.2	6480	12 ADL82848	Adl82848 Human PRO
34	1380	91.2	6480	12 ADP07302	Adp07302 Human Ccn
35	1380	91.2	6480	12 ADO20473	Ado20473 Human PRO
36	1380	91.2	6480	12 ADOL9115	Ado19115 Human PRO
37	1380	91.2	6480	12 ADOL9117	Ado19117 Human PRO
38	1380	91.2	6480	13 ADP24150	Adp24150 Human PRO
39	1380	91.2	6480	13 ADP23073	Adp23073 PRO poly
40	1380	91.2	6508	8 ABX63004	Abx63004 Human Ccn
41	1380	91.2	6508	10 ADJ56260	Adj56260 Human Ccn
42	1377	91.0	1911	2 AAQ53198	Aaq53198 Human cys
43	1374	90.8	6598	10 ADF81443	Adf81443 Leukaemia
44	1374	90.8	6598	10 ADF81444	Adf81444 Leukaemia
45	1316	87.0	6518	4 AAH57370	Aah57370 Human hea

#### ALIGNMENTS

RESULT 1

ADA02737

ID ADA02737 standard; cDNA; 870 BP.

XX AC ADA02737;

XX DT 06-NOV-2003 (first entry)

XX DE Mouse Ccn2 carcinoma associated coding sequence, SEQ ID NO:1255.

XX KW Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast;

XX KW prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;

XX KW gene; ss.

XX OS Mus sp.

XX PN WO2003057146-A2.

XX PD 17-JUL-2003.

XX PF 26-DEC-2002; 2002WO-US041414.

XX PR 26-DEC-2001; 2001US-00035832.

XX (SAGR-) SAGRES DISCOVERY.

XX PA Morris DW;

XX DR WPI; 2003-587068/55.

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 13, 2005, 20:18:51 ; Search time 3658 Seconds  
(without alignments)  
3007.265 Million cell updates/sec

Title: US-10-024-066-4  
Perfect score: 1501  
Sequence: 1 MELLCHVDPVRRVDRNL.....KSELDQASTPTDVRIDL 289

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-O=/cgm2.1/USPTO.spool.h/US10024066/runat.13072005.141000.28054/app\_query.fasta.1.910  
-DB=BST -QFMT=fastp -SUFFIX=rat -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.coi -LIST=45  
-LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptg -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10024066 @CGN 1.1 4385 @runat.13072005.141000.28054 -NCPU=6 -ICPU=3  
-NO MWAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCAPOP=6  
-FCAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: EST:\*

- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_hic:\*
- 4: gb\_est3:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_ges1:\*
- 9: gb\_ges2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1501	100.0	870	9 AY412428	Homo sapi
2	1380	91.9	870	9 AY412430	Mus muscu
3	1297	86.4	863	7 CF553381	AGENCOURT
4	1212.5	80.8	861	7 CR573818	AGENCOURT
5	1168	77.8	674	7 CR262199	170006000
6	1143	76.1	856	7 CF256675	phao01.f0
7	1132.5	75.4	783	7 CN536040	UI-M-H50
8	1129	75.2	689	6 CA316248	UI-M-FW0
9	1129	75.2	851	5 BX851524	BX851524

10	1128.5	75.2	977	5	BUS16674	AGENCOURT
11	1116.5	74.4	752	6	BY711059	BY711059
12	1113	74.2	704	4	BM790686	K-EST0070
13	1097	73.1	649	6	CD773466	AGENCOURT
14	1097	73.1	679	7	CR553173	CR553173
15	1086	72.4	904	7	CF553242	AGENCOURT
16	1080.5	72.0	848	5	BUS59877	603477919
17	1078	71.8	779	7	CN052742	Salamande
18	1059	70.6	922	5	BQ946062	AGENCOURT
19	1056	70.4	640	7	CN533599	UI-M-H00
20	1050.5	70.0	870	5	BY748469	BY748469
21	1047	69.8	635	5	CB433883	610445 MA
22	1039.5	69.3	840	5	BUS56722	UI-M-F00
23	1036.5	68.1	758	7	CN535832	UI-M-H50
24	1027.5	68.5	957	6	BY717548	BY717548
25	1026.5	68.4	851	1	AI790687	u103d12.x
26	1024	68.2	778	7	CK794714	AGENCOURT
27	1023	68.2	591	4	EG912396	602808475
28	1017	67.8	974	5	BU408763	603157571
29	1005	67.0	700	2	BE140010	EST00513
30	1003.5	66.9	748	7	CK463097	933967 MA
31	999	66.6	800	2	BF723846	EST00659
32	993.5	66.2	616	7	CF906821	A0502803-
33	993	66.2	673	1	AL631535	AGENCOURT
34	976	65.0	879	6	CB588849	AGENCOURT
35	975	65.0	925	7	CO647021	ILLUMIGEN
36	972	64.8	869	5	BP143684	BP143684
37	963.5	64.2	850	6	CB994029	AGENCOURT
38	957	63.8	814	5	BP143934	BP143934
39	952	63.4	607	4	BM790062	K-EST0069
40	952	63.4	621	6	CB215938	NISC np11
41	950.5	63.3	714	7	CK451417	904589 MA
42	950	63.3	565	1	AV589900	AV589900
43	950	63.3	867	6	CB994606	AGENCOURT
44	949	63.2	593	1	AV593772	AV593772
45	948.5	63.2	568	7	CF908102	A0518G09-

## ALIGNMENTS

RESULT 1  
AY412428  
LOCUS Homo sapiens CCND2 gene, VIRTUAL TRANSCRIPT, partial sequence, 870 bp DNA linear GSS 16-DEC-2003  
DEFINITION Homo sapiens CCND2 gene, VIRTUAL TRANSCRIPT, partial sequence, 870 bp DNA linear GSS 16-DEC-2003  
ACCESSION AY412428  
VERSION AY412428.1 GI:39768393  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 870)  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, P., Murphy, B., Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams M.D. and Cargill, M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 870)  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, P., Murphy, B., Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams M.D. and Cargill, M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.  
FEATURES  
Location/Qualifiers  
source 1 . 870

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 13, 2005, 23:40:22 ; Search time 669.5 Seconds  
(without alignments)  
2710.137 Million cell updates/sec

Title: US-10-024-066-4

Perfect score: 1501

Sequence: 1 MELLCHVEPVRRAVRDRL.....KSEDELQASTPTVRDIDL 289

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Deiop 6.0 , Deilext 7.0

Searched: 6330947 seqs, 3139163630 residues

Total number of hits satisfying chosen parameters: 12661894

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
-MODEL=frame+p2n.model -DRV=xlh  
-Q=/cgn2\_1/USPTO.spool/h/US10024066/runat\_13072005\_141002\_28138/app.query.fasta\_1.910  
-DB=Published Applications NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bloms62  
-TRANS=human40.cd1 -LIST=45 -DLOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0  
-MAXLEN=200000000 -USER=US10024066 @CEN 1 1 582 @runat\_13072005\_141002\_28138  
-NCPU=6 -ICPU=3 -NO MAP -LARGOQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*  
17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*  
19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq.\*  
20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq.\*  
21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq.\*  
22: /cgn2\_6/ptodata/1/pubpna/US10J\_NEW\_PUB.seq.\*  
23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq.\*  
24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1501	100.0	870	11	US-09-997-722-6
2	1501	100.0	873	13	US-10-024-066-3
3	1501	100.0	1898	16	US-10-210-120-14
4	1501	100.0	1898	22	US-10-909-035-14
5	1501	100.0	1911	18	US-10-641-643-1022
6	1501	100.0	6478	9	US-09-919-497-4
7	1501	100.0	6478	9	US-09-954-456-1923
8	1501	100.0	6478	9	US-09-880-107-1607
9	1501	100.0	6478	11	US-09-997-722-5
10	1501	100.0	6478	15	US-10-171-581-121
11	1501	100.0	6478	15	US-10-007-926A-461
12	1501	100.0	6478	21	US-10-843-641A-4950
13	1501	100.0	6480	17	US-10-440-464-147
14	1501	100.0	6480	20	US-10-370-715B-181
15	1501	100.0	6480	21	US-10-489-740-62
16	1501	100.0	6508	13	US-10-044-090-4
17	1501	100.0	6508	15	US-10-084-817-66
18	1380	91.9	870	11	US-09-997-722-3
19	1380	91.9	876	13	US-10-024-066-1
20	1380	91.9	1255	11	US-09-997-722-2
21	998	66.5	1053	9	US-09-778-927A-12
22	925	61.6	4242	18	US-10-641-643-1365
23	925	61.6	4244	9	US-09-964-824A-566
24	925	61.6	4244	9	US-09-954-456-1594
25	925	61.6	4244	9	US-09-967-768A-213
26	925	61.6	4244	21	US-10-843-641A-4621
27	925	61.6	4244	21	US-10-843-641A-5869
28	925	61.6	4244	21	US-10-843-641A-6358
29	925	61.6	4306	17	US-10-295-027-635
30	925	61.6	4306	18	US-10-302-812-67
31	925	61.6	4397	17	US-10-264-049-423
32	913	60.8	888	16	US-10-004-113-27
33	913	60.8	888	16	US-10-004-113-30
34	913	60.8	888	17	US-10-394-948-15
35	913	60.8	888	17	US-10-394-948-18
36	913	60.8	1256	21	US-10-690-880-10
37	913	60.8	1325	15	US-10-007-926A-10
38	913	60.8	1325	15	US-10-101-510-279
39	913	60.8	1325	16	US-10-004-113-29
40	913	60.8	1325	17	US-10-133-937-5
41	913	60.8	1325	17	US-10-172-118-661
42	913	60.8	1325	17	US-10-159-563-5
43	913	60.8	1325	17	US-10-394-948-17
44	913	60.8	1325	18	US-10-342-887-661
45	913	60.8	1454	18	US-10-152-319A-2187

# ALIGNMENTS

## RESULT 1

US-09-997-722-6  
; Sequence 6, Application US/09997722  
; Publication No. US20040072154A1  
; GENERAL INFORMATION:  
; APPLICANT: Morris, David  
; APPLICANT: Engelhard, Eric  
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER  
; FILE REFERENCE: A-71171/RMS/DCF  
; CURRENT APPLICATION NUMBER: US/09/997,722  
; PRIOR FILING DATE: 2001-11-30  
; PRIOR APPLICATION NUMBER: US 09/747,377  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 09/798,586  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 301



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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 13, 2005, 20:22:56 ; Search time 189 Seconds  
(without alignments)  
2502.032 Million cell updates/sec

Title: US-10-024-066-4  
Perfect score: 1501  
Sequence: 1 MELLCHVDVPRVAVDRNL.....KSELDQASTVDVDIDL 289

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DBV=xlh  
-Q=/cgm2\_1/USPTO\_spool\_h/US10024066/runat\_13072005\_141001\_28069/app\_query.fasta\_1.910  
-DB=Issued Patents NA -OPMT=fastap -SUFFIX=rmi -MINMATCH=0.1 -LOOPT=0  
-LOOPTXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10024066 @CGN\_1\_1\_93 @runat\_13072005\_141001\_28069 -NCFU=6 -ICFU=3  
-NO\_WMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:  
1: /cgm2\_6/ptodata/1/ina/5A\_COMB.seq:  
2: /cgm2\_6/ptodata/1/ina/5B\_COMB.seq:  
3: /cgm2\_6/ptodata/1/ina/6A\_COMB.seq:  
4: /cgm2\_6/ptodata/1/ina/6B\_COMB.seq:  
5: /cgm2\_6/ptodata/1/ina/PTUS\_COMB.seq:  
6: /cgm2\_6/ptodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1501	100.0	1129	4	US-09-920-760-3
2	1501	100.0	1911	2	US-08-246-361A-3
3	1501	100.0	1911	4	US-09-023-655-1022
4	1501	100.0	6478	4	US-09-919-497-4
5	1501	100.0	6478	4	US-09-949-016-256
6	1501	100.0	6479	4	US-09-949-016-2149
7	1471	98.0	1970	2	US-08-464-517-3
8	1471	98.0	1970	3	US-08-463-772-3
9	1471	98.0	1970	5	PCT-US93-05000-3
10	1051.5	70.1	1462	2	US-08-464-517-30
11	1051.5	70.1	1462	2	US-08-246-361A-30
12	1051.5	70.1	1462	3	US-08-463-772-30

13	1024.5	68.3	1462	5	PCT-US93-05000-30
14	927	61.8	4453	1	US-08-770-761A-4
15	927	61.8	4540	1	US-08-770-761A-6
16	927	61.8	4621	1	US-08-770-761A-1
17	925	61.6	4221	1	US-07-947-120-7
18	925	61.6	4221	1	US-08-472-893A-7
19	925	61.6	4221	3	US-08-947-492-7
20	925	61.6	4242	4	US-09-023-655-1365
21	925	61.6	4244	2	US-08-460-694-1
22	925	61.6	4244	3	US-08-460-744-1
23	925	61.6	4244	3	US-07-667-711B-1
24	913	60.8	1325	1	US-08-306-691B-51
25	911.5	60.7	1962	2	US-08-246-361A-5
26	911.5	60.7	1962	4	US-09-023-655-1023
27	911.5	60.7	2042	4	US-09-814-915A-59
28	865	57.6	1325	2	US-08-464-517-1
29	865	57.6	1325	2	US-08-246-361A-1
30	865	57.6	1325	3	US-08-463-772-1
31	865	57.6	1325	5	PCT-US93-05000-1
32	801.5	53.4	1926	3	US-08-464-517-5
33	801.5	53.4	1926	5	PCT-US93-05000-5
34	801.5	53.4	1926	5	PCT-US93-05000-5
35	522	34.8	2022	2	US-08-464-517-32
36	522	34.8	2022	2	US-08-246-361A-32
37	522	34.8	2022	3	US-08-463-772-32
38	426	28.4	1901	5	PCT-US93-05000-32
39	377.5	25.1	36302	4	US-09-949-016-11998
40	377.5	25.1	36302	4	US-09-949-016-13891
41	314.5	21.0	863	3	US-08-728-603-18
C 42	314.5	21.0	32207	2	US-08-770-379-20
C 43	314.5	21.0	32207	3	US-08-757-669A-20
C 44	314.5	21.0	32207	3	US-09-230-371A-20
45	280.5	18.7	601	4	US-09-949-016-23242

ALIGNMENTS

RESULT 1  
US-09-920-760-3  
; Sequence 3, Application US/09920760  
; Patent No. 6492173  
; GENERAL INFORMATION:  
; APPLICANT: Lex M. Cowser  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CYCLIN D2 EXPRESSION  
; FILE REFERENCE: RTS-0275  
; CURRENT APPLICATION NUMBER: US/09/920,760  
; CURRENT FILING DATE: 2001-08-01  
; NUMBER OF SEQ ID NOS: 89  
; SEQ ID NO 3  
; LENGTH: 1129  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (156)...(1025)  
US-09-920-760-3

Alignment Scores:  
Pred. No.: 2,72e-193 Length: 1129  
Score: 1501.00 Matches: 289  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-024-066-4 (1-289) x US-09-920-760-3 (1-1129)

Qy	1	MetGluLeuLeuCyHisGluValAspProValArgAlaValArgAspArgAsnLeu	20
Db	156	ATGCAGCTGCTGTGCCACGAGGTGGACCCGTCGCGAGGCGCGGACCGCAACCTG	215
Qy	21	LeuArgAspAspArgValLeuGluAsnLeuThrIleGluGluArgTyrLeuProGln	40

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 13, 2005, 17:34:44 ; Search time 596.5 Seconds  
(without alignments)  
2868.072 Million cell updates/sec

Title: US-10-024-066-4

Perfect score: 1501

Sequence: 1 MELLCHVDPRVAVRDRNL.....KSELDLQASTFDVDRIDL 289

Scoring table:

BLOSUM62	Xgapop 10.0	Xgapext 0.5
Ygapop 10.0	Ygapext 0.5	
Fgapop 6.0	Fgapext 7.0	
Delop 6.0	Delext 7.0	

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-O=/cn2.1/USPTO spool\_h/US10024066/runat 13072005 140959 28036/app query.fasta 1.910  
-DB=N Geneseg -FWT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOPEXT=0 -LOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blos62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10024066 @CN 1.1 586 @runat 13072005 140959 28036 -NCPU=6 -ICPU=3  
-NO MAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1:	Geneseg16Dec04.*
2:	Geneseg1980s.*
3:	Geneseg1990s.*
4:	Geneseg2000s.*
5:	Geneseg2001as.*
6:	Geneseg2001bs.*
7:	Geneseg2002as.*
8:	Geneseg2002bs.*
9:	Geneseg2003as.*
10:	Geneseg2003bs.*
11:	Geneseg2003ds.*
12:	Geneseg2004as.*
13:	Geneseg2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1501	100.0	870	9 ADA02740	Ada02740 Human CCN
2	1501	100.0	870	10 ADB72478	Adb72478 Human CCN
3	1501	100.0	870	10 ADC85220	Adc85220 Human Ccn
4	1501	100.0	870	12 ADM74335	Adm74335 Human car
5	1501	100.0	873	5 AAD02407	Aad02407 Human cnc

6	1501	100.0	1129	10 ACA60565	Acac60565 DNA encod
7	1501	100.0	1898	10 ADD18442	Add18442 Human pro
8	1501	100.0	1911	2 AAD31874	Aad31874 Cyclin D2
9	1501	100.0	1911	11 ADI31696	Adi31696 Human cDN
10	1501	100.0	6478	6 ABK35484	Abk35484 Human end
11	1501	100.0	6478	6 ABL66613	AbL66613 Lung canc
12	1501	100.0	6478	6 ABV94470	Abv94470 Breast ca
13	1501	100.0	6478	6 ABN95109	Abn95109 Gene #160
14	1501	100.0	6478	9 ADA02739	Ada02739 Human CCN
15	1501	100.0	6478	10 ADB72477	Adb72477 Human CCN
16	1501	100.0	6478	10 ADC85219	Adc85219 Human Ccn
17	1501	100.0	6478	10 ADF81445	Adf81445 Leukaemia
18	1501	100.0	6478	10 ADH28853	Adh28853 Human chr
19	1501	100.0	6478	12 ADM74334	Adm74334 Human car
20	1501	100.0	6478	12 ADO19119	Ado19119 Human PRO
21	1501	100.0	6480	8 ACF34507	Acf34507 Gene enco
22	1501	100.0	6480	10 ADF76507	Adf76507 Novel hum
23	1501	100.0	6480	12 ADH17148	Adh17148 Human cnc
24	1501	100.0	6480	12 ADL82848	Adl82848 Human PRO
25	1501	100.0	6480	12 ADP07302	Adp07302 Human CCN
26	1501	100.0	6480	12 ADO20473	Ado20473 Human PRO
27	1501	100.0	6480	12 ADO19115	Ado19115 Human PRO
28	1501	100.0	6480	12 ADO19117	Ado19117 Human PRO
29	1501	100.0	6480	13 ADP54150	Adp54150 Human PRO
30	1501	100.0	6480	13 ADP23073	Adp23073 PRO poly
31	1501	100.0	6508	8 ABX63004	Abx63004 Human cDN
32	1501	100.0	6508	10 ADJ56260	Adj56260 Human cDN
33	1495	99.6	6598	10 ADF81443	Adf81443 Leukaemia
34	1495	99.6	6598	10 ADF81444	Adf81444 Leukaemia
35	1491	99.3	1911	2 AAO53198	Aao53198 Human cnc
36	1436	95.7	6518	4 AHS57370	Aah57370 Human hea
37	1380	91.9	870	9 ADA02737	Ada02737 Mouse Ccn
38	1380	91.9	870	10 ADB72475	Adb72475 Mouse Ccn
39	1380	91.9	870	10 ADC85217	Adc85217 Mouse Ccn
40	1380	91.9	870	12 ADM74332	Adm74332 Murine ca
41	1380	91.9	876	5 AAD02406	Aad02406 Mouse cnc
42	1380	91.9	1255	9 ADA02736	Ada02736 Mouse Ccn
43	1380	91.9	1255	10 ADB72474	Adb72474 Mouse Ccn
44	1380	91.9	1255	10 ADC85216	Adc85216 Mouse Ccn
45	1380	91.9	1255	12 ADM74331	Adm74331 Murine ca

## ALIGNMENTS

RESULT 1  
ADA02740

ID ADA02740 standard; cDNA; 870 BP.

AC ADA02740;

DT 06-NOV-2003 (first entry)

DE Human CCND2 carcinoma associated coding sequence, SEQ ID NO:1258.

XX Human; carcinoma associated; oncogene; carcinoma; cancer; breast;  
KW prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;  
XX gene; ss.  
XX Homo sapiens.

OS Homo sapiens.

XX WO2003057146-A2.

PN 17-JUL-2003.

PD 26-DEC-2002; 2002WO-US041414.

PP 26-DEC-2001; 2001US-00035832.

PR (SAGR-) SAGRES DISCOVERY.

PA PA

XX PI Morris DW;

XX DR WPI; 2003-587068/55.

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 13, 2005, 19:05:08 ; Search time 4889.5 Seconds

(without alignments)  
2864.006 Million cell updates/sec

Title: US-10-024-066-4

Perfect score: 1501

Sequence: 1 MELLCHVDPVRAVRDNL.....KSEDELQASTPTDVRIDL 289

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPTO.spool\_h/US10024066/runat\_13072005\_140959\_28043/app\_query.fasta\_1.910  
-DB=GenEmbl -OPT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10024066 @CGN 1 1 4930 @runat\_13072005\_140959\_28043 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGIOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.\*  
1: gb.ba.\*  
2: gb.htg.\*  
3: gb.in.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1501	100.0	870	6 AX695631 Sequence
2	1501	100.0	1129	6 AR266191 Sequence
3	1501	100.0	1129	9 HSCVCD2 X68452 H.sapiens m
4	1501	100.0	1344	9 BC010958 Homo sapi

5	1501	100.0	1911	6	AR093074	Sequence
6	1501	100.0	1911	6	AR380477	Sequence
7	1501	100.0	1911	6	BD079953	Use relat
8	1501	100.0	1911	9	HUMCCND2A	M30813 Human D-typ
9	1501	100.0	6478	6	AX334441	Sequence
10	1501	100.0	6478	6	AX408960	Sequence
11	1501	100.0	6478	6	AX587991	Sequence
12	1501	100.0	6478	6	AX695630	Sequence
13	1501	100.0	6478	6	AX779844	Sequence
14	1501	100.0	6478	9	HUMRSC289	D13639 Homo sapien
15	1495	99.6	6598	6	AX779842	Sequence
16	1495	99.6	6598	6	AX779843	Sequence
17	1471	98.0	1970	6	AR034831	Sequence
18	1402.5	92.4	1230	4	AB046174	Sus scrofa
19	1392.5	92.8	1415	10	RATCYCLD2A	L09752 Rat cyclin
20	1380	91.9	870	6	AX695628	Sequence
21	1380	91.9	1034	10	MUSCYL2A	M86182 Mouse cycli
22	1380	91.9	1255	6	AX695627	Sequence
23	1380	91.9	1255	10	MUSDCYC	M83749 Mouse D-typ
24	1380	91.9	2037	10	BC049086	Mus muscu
25	1379.5	91.9	1120	10	RATCLND2	D16308 Rattus norv
26	1256	83.7	1173	5	GGU28980	U28980 Gallus gall
27	1236	82.3	1588	5	XLVCYCD2	X89476 X.laavis mR
28	1236	82.3	2038	5	XLVCYCD2	X83503 X.laavis mR
29	1083.5	72.2	170682	2	AC073256	Homo sapi
30	1067.5	71.1	160945	9	AP003420	Homo sapi
31	1066.5	71.1	116273	2	AP000596	Homo sapi
32	1062.5	70.8	169776	9	AP001880	Homo sapi
33	1062.5	70.8	169777	2	AC090778	Homo sapi
34	1058.5	70.5	185404	2	AC025409	Homo sapi
35	1051.5	70.1	1462	6	AR034838	Sequence
36	1051.5	70.1	1462	6	AR033081	Sequence
37	1051.5	70.1	1462	6	BD079960	Use relat
38	1024.5	68.3	1462	9	HUMCCND2PS	M91003 Human pseud
39	953.5	63.5	2248	5	AJ720095	Gallus ga
40	927	61.8	4453	6	AR043602	Sequence
41	927	61.8	4540	6	AR043603	Sequence
42	927	61.8	4621	6	AR043601	Sequence
43	925	61.6	885	9	CR542099	Homo sapi
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45	925	61.6	1248	9	BC014078	Homo sapi

#### ALIGNMENTS

RESULT 1  
AX695631  
LOCUS AX695631 870 bp DNA linear PAT 31-MAR-2003  
DEFINITION Sequence 1258 from Patent WO03008583.  
ACCESSION AX695631  
VERSION AX695631.1 GI:29418783  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Morris, D.W. and Engelhard, E.K.  
TITLE Novel compositions and methods for cancer  
JOURNAL Patent: WO 03008583-A 1258 30-JAN-2003;  
Sagres Discovery (US)  
FEATURES  
source  
1. .870  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Alignment Scores:  
Pred. No.: 9.43e-147 Length: 870  
Score: 1501.00 Matches: 289  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 13, 2005, 19:05:08 ; Search time 4889.5 Seconds  
(without alignments)  
2864.006 Million cell updates/sec

Title: US-10-024-066-2

Perfect score: 1513

Sequence: 1 MELLCEVDPRRAVPRNL.....KSVEDPDQATPTDVRVDL 289

Scoring table:

BLOSUM62	
Xgapop 10.0, Xgapext 0.5	
Ygapop 10.0, Ygapext 0.5	
Fgapop 6.0, Fgapext 7.0	
Delop 6.0, Delext 7.0	

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh  
-Q=/cgn2.1/USPTO.spool.h/US10024066/runat.13072005.140959.28043/app.query.fasta.1.910  
-DB=GenEmbl -OFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10024066 @CGN 1.1 4930 @runat.13072005.140959.28043 -NCPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -PGAPOP=6  
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.\*  
1: gb.ba.\*  
2: gb.htg.\*  
3: gb.in.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1513	100.0	870	6	AX695628 Sequence
2	1513	100.0	1034	10	MUSC12A
3	1513	100.0	1255	6	AX695627
4	1513	100.0	1255	10	MUSDCYC

5	1513	100.0	2037	10	BC049086	BC049086 Mus muscu
6	1482.5	98.0	1415	10	RATCYCLD2A	L09752 Rat cyclin
7	1469.5	97.1	1120	10	RATCLND2	D16308 Rattus norv
8	1380	91.2	870	6	AX695631	AX695631 Sequence
9	1380	91.2	1129	6	AR266191	AR266191 Sequence
10	1380	91.2	1129	9	HSCYCD2	X58452 H.sapiens m
11	1380	91.2	1344	9	BC010958	BC010958 Homo sapi
12	1380	91.2	1911	6	AR093074	AR093074 Sequence
13	1380	91.2	1911	6	AR380477	AR380477 Sequence
14	1380	91.2	1911	6	BD079953	BD079953 Use relat
15	1380	91.2	1911	9	HUMCCND2A	M08113 Human D-typ
16	1380	91.2	6478	6	AX334441	AX334441 Sequence
17	1380	91.2	6478	6	AX408960	AX408960 Sequence
18	1380	91.2	6478	6	AX587991	AX587991 Sequence
19	1380	91.2	6478	6	AX695630	AX695630 Sequence
20	1380	91.2	6478	6	AX779844	AX779844 Sequence
21	1380	91.2	6478	9	HUMRSC289	D13639 Homo sapien
22	1374	90.8	6598	6	AX779842	AX779842 Sequence
23	1374	90.8	6598	6	AX779843	AX779843 Sequence
24	1360.5	89.9	1230	4	AB046174	AB046174 Sus scrof
25	1357	89.7	1970	6	AR034831	AR034831 Sequence
26	1267	83.7	1173	5	GGU28980	U28980 Gallus gall
27	1225	81.0	1588	5	XLCYCLND2	X89476 X.lauevis mR
28	1225	81.0	2038	5	XLCYCD2	X83503 X.lauevis mR
29	1007.5	66.6	170682	2	AC073256	AC073256 Homo sapi
30	991.5	65.5	160945	9	AP003420	AP003420 Homo sapi
31	988.5	65.3	116273	2	AP000596	AP000596 Homo sapi
32	986.5	65.2	169776	9	AP001880	AP001880 Homo sapi
33	986.5	65.2	169777	2	AC090778	AC090778 Homo sapi
34	979.5	64.7	185404	2	AC025409	AC025409 Homo sapi
35	975.5	64.5	1462	6	AR034838	AR034838 Sequence
36	975.5	64.5	1462	6	AR033081	AR033081 Sequence
37	975.5	64.5	1462	6	BD079960	BD079960 Use relat
38	961	63.5	1555	5	BC074566	BC074566 Xenopus t
39	958	63.3	885	9	CR542099	CR542099 Homo sapi
40	958	63.3	888	9	CR536538	CR536538 Homo sapi
41	958	63.3	1248	9	BC014078	BC014078 Homo sapi
42	958	63.3	1251	9	BC000076	BC000076 Homo sapi
43	958	63.3	1251	9	BC001501	BC001501 Homo sapi
44	958	63.3	1265	6	CQ723408	CQ723408 Sequence
45	958	63.3	1464	9	BC025302	BC025302 Homo sapi

#### ALIGNMENTS

RESULT 1	AX695628	Sequence 1255 from Patent WO03008583.	870 bp	DNA	linear	PAT 31-MAR-2003
LOCUS	AX695628					
DEFINITION	Sequence 1255 from Patent WO03008583.					
ACCESSION	AX695628					
VERSION	AX695628.1	GI:29418780				
KEYWORDS						
SOURCE	Mus musculus (house mouse)					
ORGANISM	Mus musculus					
REFERENCE	1					
AUTHORS	Morris, D.W. and Engelhard, E.K.					
TITLE	Novel compositions and methods for cancer					
JOURNAL	Patent: WO 03008583-A 1255 30-JAN-2003;					
FEATURES	Sagres Discovery (US)					
source	Location/Qualifiers					
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	/db_xref="taxon:10090"					
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Alignment Scores:						
Pred. No.:	8.03e-155					Length: 870
Score:	1513.00					Matches: 289
Percent Similarity:	100.00%					Conservative: 0
Best Local Similarity:	100.00%					Mismatches: 0